Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) A method for providing information about biological molecules, comprising the acts of:

receiving a user selection of one or more probe set identifiers that identify ~~probe sets of~~ one or more probe-sets disposed on one or more ~~synthesized or spotted~~ probe arrays ~~capable of detecting the biological molecules~~ and one or more intensity values detected from each probe-set, wherein the user performs the selection using a client side interface that is received over an internet network by a host side;

determining one or more alternative splice variants ~~based at least in part upon~~ by iteratively fitting the probe-set identifiers and intensity values to a plurality of models of known genomic structure associated with the alternative splice variants ~~the one or more probe set identifiers~~, wherein the fit of one or more of the models to the probe-set identifiers and the intensity values indicates the presence of the alternative splice variants and at least one of the probe arrays or at least one of the probe sets detects ~~is constructed and arranged to detect or measure any one or any combination of gene expression, genotype, SNP, haplotype, or targets including antibodies, cell membrane receptors, monoclonal antibodies and antisera reactive with specific antigenic determinants, drugs, oligonucleotides,~~ nucleic acids~~, peptides, proteins, cofactors, lectins, sugars, polysaccharides, cells, cellular membranes, or organelles~~;

correlating at least one alternative splice variant with at least one annotation datum; and

providing to the user, over ~~a~~ the internet network, a graphical representation of the at least one alternative splice variant and the correlated annotation datum.

2. (Currently Amended) The method of claim 1, wherein:

one or more of the probe arrays is ~~constructed and arranged to diagnose~~ capable of diagnosing a disease or medical condition.

3. (Currently Amended) A method, comprising the acts of:

determining one or more alternative splice variants ~~based at least in part upon~~ by iteratively fitting one or more user selected probe set identifiers that identify ~~probe sets~~ one or more probe-sets disposed on one or more probe arrays and one or more intensity values detected from each probe-set to a plurality of models of known genomic structure associated with the alternative splice variants, wherein the fit of one or more of the models to the probe set identifiers and the intensity values indicates the presence of the alternative splice variants ~~capable of detecting biological molecules~~;

correlating at least one alternative splice variant with at least one annotation datum; and

~~enabling for display~~ providing to a user over an internet network a graphical representation of the at least one alternative splice variant and the correlated annotation datum.

4. (Currently Amended) The method of claim 3, further comprising the act of:

receiving ~~from a~~ the user selection of the one or more probe set identifiers.

5. (Currently Amended) The method of claim 4, wherein:

the act of receiving includes the acts of the user originating the selection from a user computer, transmission of the selection over ~~the Internet~~ the internet network, and receipt of the selection at an Internet server.

6. (Cancelled)

7. (Currently Amended) The method of claim 3, wherein:

the ~~probe sets include~~ one or more probe arrays comprise probes disposed on or in a support comprising beads, resins, gels, or microspheres.

8.-10. (Cancelled)

11. (Original) The method of claim 3, wherein:

the act of correlating includes correlating the at least one alternative splice variant with a gene and correlating the gene with the at least one annotation datum.

12. (Original) The method of claim 3, wherein:

the act of correlating includes correlating the at least one alternative splice variant with at least one other alternative splice variant of their common gene and correlating the at least one other alternative splice variant with the at least one annotation datum.

13. (Currently Amended) The method of claim 3, wherein:

the graphical representation of the at least one alternative splice variant or of the at least one annotation datum ~~is constructed and arranged to enable~~ enables semantic zooming wherein magnification is determined~~, at least in part,~~ on a user zoom selection.

14. (Original) The method of claim 13, wherein:

the annotation datum includes sequence information displayed on a sequence axis, and the semantic zooming is along a single dimension corresponding to the sequence axis.

15. (Currently Amended) The method of claim [[13]]3, wherein:

the graphical representation of the at least one alternative splice variant or of the at least one annotation datum is organized into a plurality of adjustable tiers that are ~~constructed and arranged for display~~ represented so as to be capable of being collapsed, moved, or hidden in response to user tier selection.

16. (Currently Amended) The method of claim 3, wherein:

the graphical representation of the at least one annotation datum is ~~constructed and arranged for display based, at least in part, on~~ represented in response to a user

selection of ~~one or more of a genomic, primary transcript,~~ an mRNA~~, or protein display type~~.

17. (Currently Amended) The method of claim 3, wherein:

the at least one annotation datum includes ~~any one or any combination of genomic sequence; presence or relative abundance of alternative splice variants; exon arrangement, content, or sequence; intron arrangement, content, or sequence; frequency of exon usage in two or more of the alternative splice variants; isoform identification; primary transcript,~~ mRNA ~~or other RNA identification, function, structure, or sequence; protein, protein domain, or protein motif identification, function, structure, or sequence; gene identification, function, structure, or sequence for a gene corresponding to the at least one alternative splice variant; one or more start or stop sites; 5' and 3' untranslated regions; coding regions; protein-based annotations of the coding regions; start and stop codons; 5' transcriptional control elements; 3' polyadenylation signals; splice site boundaries; probe arrangement, content, or sequence; or expression level data corresponding to one or more probes of the probe sets~~.

18. (Currently Amended) The method of claim 3, wherein:

the act of ~~enabling for display~~ providing the graphical representation includes a representation of an alignment ~~aligning the representation~~ of a first alternative splice variant with a second alternative splice variant, wherein the first and second alternative splice variants are variants of a same gene.

19. (Currently Amended) The method of claim 18, wherein:

the ~~aligning is based, at least in part, on sequences~~ alignment of the first and second alternative splice variants comprises a ~~compared~~ comparison of the first and second alternative splice variants to genomic sequence or sequence of the same gene.

20. (Currently Amended) The method of claim 3, wherein:

the act of ~~enabling for display~~ providing the graphical representation includes graphically associating the alternative splice variant and the annotation datum.

21. (Currently Amended) The method of claim 3, wherein:

the act of ~~enabling for display~~ providing the graphical representation includes ~~enabling separate display of~~ representing a plurality of annotation data in a plurality of panes of a single graphical user interface.

22.-23. (Cancelled)

24. (Original) The method of claim 3, wherein:

the probe sets comprise probes constructed and arranged to detect mRNA expression.

25. (Currently Amended) The method of claim [[3]]24, wherein:

the probes comprise exon probes or junction probes.

26.-27 (Cancelled)

28. (Currently Amended) A system comprising:

an alternative splice variant evaluator ~~constructed and arranged to determine~~ that determines one or more alternative splice variants ~~based at least in part upon~~ by iteratively fitting one or more user selected probe set identifiers that identify ~~probe sets~~ one or more probe-sets disposed on one or more probe arrays and one or more intensity values detected from each probe-set to a plurality of models of known genomic structure associated with the alternative splice variants, wherein the fit of one or more of the models to the probe-set identifiers and the intensity values indicates the presence of the alternative splice variants ~~capable of detecting biological molecules~~;

an alternative splice variant data storage and annotation data correlator ~~constructed and arranged to correlate~~ that correlates at least one alternative splice variant with at least one annotation datum; and

a user-service manager ~~constructed and arranged to enable for display~~ that provides to a user over an internet network a graphical representation of the at least one alternative splice variant and the correlated annotation datum.

29. (Currently Amended) The system of claim 28, further comprising:

an input manager ~~constructed and arranged to receive from a~~ that receives the user a selection of the one or more probe set identifiers.

30. (Currently Amended) The system of claim 29, wherein:

the input manager receives the user selection over the Internet network .

31. (Currently Amended) The system of claim 28, wherein:

the probe sets include probes of a probe array ~~constructed and arranged to~~ that detect or measure ~~any one or any combination of gene expression, genotype, SNP, haplotype, or targets including antibodies, cell membrane receptors, monoclonal antibodies and antisera reactive with specific antigenic determinants, drugs, oligonucleotides,~~ nucleic acids~~, peptides, proteins, cofactors, lectins, sugars, polysaccharides, cells, cellular membranes, or organelles~~.

32. (Currently Amended) The system of claim 28, wherein:

the graphical representation of the at least one alternative splice variant or of the at least one annotation datum ~~is constructed and arranged to enable~~ enables semantic zooming wherein magnification is determined~~, at least in part,~~ on a user zoom selection.

33. (Currently Amended) The system of claim 28, wherein:

the representation of the at least one annotation datum is ~~constructed and arranged for display based, at least in part, on~~ represented in response to a user selection of ~~one or more of a genomic, primary transcript,~~ an mRNA~~, or protein display type~~.

34. (Currently Amended) The system of claim 28, wherein:

the at least one annotation datum includes ~~any one or any combination of genomic sequence; presence or relative abundance of alternative splice variants; exon~~

~~arrangement, content, or sequence; intron arrangement, content, or sequence; frequency of exon usage in two or more of the alternative splice variants; isoform identification; primary transcript,~~ mRNA ~~or other RNA identification, function, structure, or sequence; protein, protein domain, or protein motif identification, function, structure, or sequence; gene identification, function, structure, or sequence for a gene corresponding to the at least one alternative splice variant; one or more start or stop sites; 5' and 3' untranslated regions; coding regions; protein-based annotations of the coding regions; start and stop codons; 5' transcriptional control elements; 3' polyadenylation signals; splice site boundaries; probe arrangement, content, or sequence; or expression level data corresponding to one or more probes of the probe sets~~.

35. (Currently Amended) The system of claim 28, wherein:

the ~~user service manager further is constructed and arranged to align the representation~~ graphical representation includes a representation of an alignment of a first alternative splice variant with a second alternative splice variant, wherein the first and second alternative splice variants are variants of a same gene.

36. (Currently Amended) The system of claim 35, wherein:

the ~~aligning is based, at least in part, on sequences~~ alignment of the first and second alternative splice variants comprises a ~~compared~~ comparison of the first and second alternative splice variants to genomic sequence or sequence of the same gene.

37. (Currently Amended) The system of claim 28, wherein:

the ~~user service manager further is constructed and arranged to~~ graphical representation includes graphically ~~associate~~ associating the alternative splice variant and the annotation datum.

38.-39. (Cancelled)

40. (Original) The system of claim 28, wherein:

the probe sets comprise probes constructed and arranged to detect mRNA expression.

41. (Currently Amended) The system of claim [[28]]40, wherein:

the probes comprise exon probes or junction probes.

42. (Cancelled)

43. (Currently Amended) A genomic web portal, comprising:

an input manager ~~constructed and arranged to receive from~~ that receives a user ~~over the Internet a~~ selection of one or more probe set identifiers that identify ~~probe sets capable of~~ one or more probe-sets disposed on one or more probe arrays ~~detecting biological molecules~~ and one or more ~~hybridization~~ intensity values detected from each probe-set , wherein the user performs the selection using a client side interface that is received over an internet network by a host side ~~corresponding to the one or more probe~~

~~set identifiers, wherein the hybridization intensity values are produced from biological probe array experiments~~;

an alternative splice variant evaluator ~~constructed and arranged to determine~~ that determines one or more alternative splice variants ~~based at least in part upon~~ by iteratively fitting the probe-set identifiers and intensity values to a plurality of models of known genomic structure associated with the alternative splice variants ~~one or more probe set identifiers and their corresponding hybridization intensity values~~, wherein the fit of one or more of the models to the probe-set identifiers and the intensity values indicates the presence of the alternative splice variants;

an alternative splice variant data storage and annotation data correlator ~~constructed and arranged to correlate~~ that correlates at least one alternative splice variant with at least one annotation datum;

~~a user service manager constructed and arranged to enable for display a representation of the at least one alternative splice variant and the correlated annotation datum; and~~

an output manager ~~constructed and arranged to send~~ that provides to the user over the Internet network ~~the~~ a graphical representation of the at least one alternative splice variant and the correlated annotation datum.

44. (Currently Amended) The genomic web portal of claim 43, wherein:

the graphical representation of the at least one annotation datum ~~is constructed and arranged for display based, at least in part, on~~ comprises a user selection of ~~one or more of a genomic, primary transcript,~~ an mRNA~~, or protein display type~~.

45. (Currently Amended) The genomic web portal of claim 43, wherein:

the at least one annotation datum includes ~~any one or any combination of genomic sequence; presence or relative abundance of alternative splice variants; exon arrangement, content, or sequence; intron arrangement, content, or sequence; frequency of exon usage in two or more of the alternative splice variants; isoform identification; primary transcript,~~ mRNA ~~or other RNA identification, function, structure, or sequence; protein, protein domain, or protein motif identification, function, structure, or sequence; gene identification, function, structure, or sequence for a gene corresponding to the at least one alternative splice variant; one or more start or stop sites; 5' and 3' untranslated regions; coding regions; protein-based annotations of the coding regions; start and stop codons; 5' transcriptional control elements; 3' polyadenylation signals; splice site boundaries; probe arrangement, content, or sequence; or expression level data corresponding to one or more probes of the probe sets~~.